

73893

STIC-Biotech/ChemLib

Fr m: Yaen, Christopher
Sent: Wednesday, August 21, 2002 5:51 PM
To: STIC-Biotech/ChemLib
Subject: 09811118

could you please run a seq search on seq id no 1 and 2 both regular and oligo

thanks

Christopher Yaen
Patent Examiner
US PTO
Art Unit 1642
CM1-Rm 8E18
Mail Box 8E12
703-305-3586

CRIE

Point of Contact:
Toby Port
Technical Info. Specialist
CM1 6A04
703-308-3534

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 8/23
Date Completed: 8/26
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: 2
AA Sequences: 2
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: es
WWW/Internet: _____
Other (specify): _____

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 23, 2002, 14:39:58 ; Search time 11.94 Seconds
(without alignments)
606.412 Million cell updates/sec

Title: US-09-811-118-1

Perfect score: 187
Sequence: 1 MVATVAAAMLMLMAACAQ.....VRLQITALVRLKLLKREDL 187

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size: 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	7.0	167	1	GSHE_HELAN
2	11	5.9	169	1	GPO_STNY3
3	10	5.3	163	1	GSHE_CAEEL
4	9	4.8	17	1	GSHE_PINPS
5	9	4.8	163	1	GSHE_CAEEL
6	9	4.8	167	1	GSHE_CITSL
7	9	4.8	169	1	GSHE_SCHMA
8	9	4.8	169	1	GSHE_NICST
9	9	4.8	180	1	GSHE_HELAN
10	9	4.8	197	1	GSHE_HUMAN
11	9	4.8	197	1	GSHE_MOUSE
12	9	4.8	197	1	GSHE_PIG
13	9	4.8	197	1	GSHE_RAT
14	9	4.8	242	1	GSHE_ARATH
15	8	4.3	122	1	GSHE_DIRIM
16	8	3.7	122	1	GSHE_HUMAN
17	7	3.7	122	1	RL7_PSEAE
18	7	3.7	155	1	YEH3_YEAST
19	7	3.7	158	1	GSHE_SCHRO
20	7	3.7	162	1	GSHE_YEAST
21	7	3.7	163	1	GSHE_YEAST
22	7	3.7	183	1	BTUE_ECOLI
23	7	3.7	190	1	GSHE_HUMAN
24	7	3.7	190	1	GSHE_MOUSE
25	7	3.7	200	1	GSHE_RABIT
26	7	3.7	201	1	GSHE_HUMAN
27	7	3.7	201	1	GSHE_MOUSE
28	7	3.7	205	1	GSHE_RAT
29	7	3.7	211	1	GSHE_BOVIN
30	7	3.7	219	1	KAD_TREPA
31	7	3.7	219	1	GSHE_PIG
32	7	3.7	221	1	GSHE_CANFA
33	7	3.7	221	1	GSHE_HUMAN

34	7	3.7	221	1	GSHE_MACFA
35	7	3.7	221	1	GSHE_MOUSE
36	7	3.7	221	1	GSHE_RAT
37	7	3.7	221	1	GSHE_RAT
38	7	3.7	224	1	GSHE_CAEEL
39	7	3.7	226	1	GSHE_BOVIN
40	7	3.7	226	1	GSHE_HUMAN
41	7	3.7	226	1	GSHE_RAT
42	7	3.7	284	1	MP5B_PHLPR
43	7	3.7	294	1	MP53_PHAQA
44	7	3.7	316	1	TAL_HARIN
45	7	3.7	320	1	MP51_PHAQA

ALIGNMENTS

RESULT	ID	GSHE_HELAN	STANDARD	PRT	167 AA.
AC	023970:				
DT	15-DEC-1998 (Rel. 37, Last sequence update)				
DT	15-DEC-1998 (Rel. 37, Last sequence update)				
DT	30-MAY-2000 (Rel. 39, Last annotation update)				
DE	Glutathione peroxidase 1 (EC 1.11.1.9).				
GN	GPXRA-1.				
OS	Helianthus annuus (Common sunflower).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
OC	Asteridae; eusterids II; Asterales; Asteraceae; Asteroideae;				
OC	Heliantheae; Helianthus.				
OX	NCBI_TaxID=4232;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Drevet J.R., Gagne G., Tourvieille de Labrouhe D., Nicolas P.,				
RA	Dufaire J.P., Ledoit G., Roedel-Drevet P.;				
RL	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.				
CC	-1- FUNCTION: MAY CONSTITUTE A GLUTATHIONE PEROXIDASE-LIKE				
CC	PROTECTIVE SYSTEM AGAINST OXIDATIVE STRESSES.				
CC	-1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized				
CC	glutathione + 2 H(2)O.				
CC	-1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
CC	-----				
DR	EMBL: Y14439; CAAT4775.1; -				
DR	HSSP: P00435; IGP1.				
DR	InterPro: IPR000889; Glut_peroxidase.				
DR	Pfam: PF00255; GSHPX.1.				
DR	PRINTS: PR01011; GLUTPROXASE.				
DR	PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.				
DR	PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.				
KW	Oxidoreductase; Peroxidase.				
FT	ACT_SITE 41				
FT	ACT_SITE 41				
SQ	SEQUENCE 167 AA; 18842 MW; CF5AC7ACCT6558C9 CRC64;				

Query Match 7 0%; Score 13; DB 1; Length 167;

Best Local Similarity 100.0%; Pred. No. 5.9e-06;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 LAEPNQGQGP 94
|||||
DB 66 LAEPNQGQGP 78

RESULT 2

GPO_SVNY3
ID GPO_SVNY3 STANDARD; PRT; 169 AA.
AC P74250;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative glutathione peroxidase (EC 1.11.1.9).
GN SLR1171.
OS Synechocystis sp. (strain PCC 6803)
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naito K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized
CC glutathione + 2 H(2)O.
CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC
DR EMBL: D90913; BAA18344.1; -
DR HSSP: P00435; 1GPI.
DR InterPro: IPR000889; Glut_peroxidase.
DR Pfam: PF00255; GSHpx.1.
DR PRINTS: PR01011; GLUTPROXADASE.
DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
KW Peroxidase; Oxidoreductase; Complete proteome.
FT ACT SITE 41
FT ACT SITE 41
SO SEQUENCE 169 AA; 18452 MW; 0DC382089FCE39E2 CRC64;

Query Match 5.9%; Score 11; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 84 FPCNFGQDEP 94
DB 67 FPCNFGQDEP 77
IIIIIIIIII

RESULT 3
GSHD_CAMEL
ID GSHD_CAMEL STANDARD; PRT; 163 AA.
AC 86827;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Probable glutathione peroxidase R05H10.5 (EC 1.11.1.9).
GN R05H10.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL NZ;
RA McMurray A.;

RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MAY CONSTITUTE A GLUTATHIONE PEROXIDASE-LIKE
CC PROTECTIVE SYSTEM AGAINST OXIDATIVE STRESSES (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized
CC glutathione + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC
DR EMBL: 283119; CAB05581.1; -
DR HSSP: P00435; 1GPI.
DR WormPep: R05H10.5; CE18107.
DR InterPro: IPR000889; Glut_peroxidase.
DR Pfam: PF00255; GSHpx.1.
DR PRINTS: PR01011; GLUTPROXADASE.
DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
KW Oxidoreductase; Peroxidase.
FT ACT SITE 36
FT ACT SITE 36
SO SEQUENCE 163 AA; 18152 MW; 8D5FE6DF96D212CA CRC64;

Query Match 5.3%; Score 10; DB 1; Length 163;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 VLAFCNORG 90
DB 60 VLAFCNORG 69
IIIIIIIIII

RESULT 4
GSHX_PINPS
ID GSHX_PINPS STANDARD; PRT; 17 AA.
AC P81087;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Glutathione peroxidase homolog (EC 1.11.1.9) (Water stress responsive
DE proteins 8 and 9) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=96418576; PubMed=9747804;
RX Costa P., Bahman N., Frigerio J.-M., Kremer A., Plomion C.;
RX "Water-deficit-responsive proteins in maritime pine.";
RX Plant Mol. Biol. 38:587-596(1998).
RN [2]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RX Costa P., Plomion C., Bauw G., Dubos C., Bahman N., Kremer A.,
RX Frigerio J.-M., Plomion C.;
RX "Separation and characterization of needle and xylem maritime pine
RX proteins.";
RT Electrophoresis 20:1098-1108(1999).
CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized
CC glutathione + 2 H(2)O.
CC -1- INDUCTION: BY WATER STRESS.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC 5.6 TO 6.7, ITS MW IS: 20 TO 23 KDa.
CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.

DR HSSP; P00435; 1GP1.
 DR InterPro: IPR000889; Glut_peroxidase.
 DR Pfam: PF00255; GSHPX; 1.
 DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; PARTIAL.
 DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
 KW Peroxidase; Oxidoreductase.
 FT NON_TER 1 17
 FT 17 17
 SQ SEQUENCE 17 AA; 1943 MW; 4D245E9B57868C1 CRC64;

Query Match 4.8%; Score 9; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFCPNOFG 90
 DB 9 LAFCPNOFG 17

RESULT 5
 GSHC_CAEEL STANDARD; PRT; 163 AA.
 ID GSHC_CAEEL
 AC 002621;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Probable glutathione peroxidase F26E4.12 (EC 1.11.1.9).
 GN F26E4.12.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Lightning J.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MAY CONSTITUTE A GLUTATHIONE PEROXIDASE-LIKE
 CC PROTECTIVE SYSTEM AGAINST OXIDATIVE STRESSES (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized
 CC glutathione + 2 H(2)O.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Z61070; CAB03004.1; -.
 DR HSSP; P00435; 1GP1.
 DR WormBep: F26E4.12; CE09696.
 DR InterPro: IPR000889; Glut_peroxidase.
 DR Pfam: PF00255; GSHPX; 1.
 DR PRINTS: PRO1011; GLUTPROXDASE.
 DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
 DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
 KW Oxidoreductase; Peroxidase.
 FT ACT_SITE 36 36
 FT 36 36 BY SIMILARITY.
 SQ SEQUENCE 163 AA; 18424 MW; 441535A92DC4330F CRC64;

Query Match 4.8%; Score 9; DB 1; Length 163;
 Best Local Similarity 100.0%; Pred. No. 0.078;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 VLAFCPNOF 89
 DB 60 VLAFCPNOF 68

RESULT 6
 GSHZ_CITSI STANDARD; PRT; 167 AA.
 ID GSHZ_CITSI
 AC 006652;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Glutathione peroxidase homolog (EC 1.11.1.9) (Salt-associated
 DE protein).
 GN CSA.
 OS Citrus sinensis (Sweet orange).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustosids II; Sapindales; Rutaceae; Citrus.
 OX NCBI_TaxID=2711;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE-93222490; Pubmed-8467085;
 RA Holland D., Ben-Hayim G., Faltin Z., Camoin L., Strosberg A.D.,
 RA Eshdat Y.;
 RT "Molecular characterization of salt-stress-associated protein in
 RT citrus: protein and cDNA sequence homology to mammalian glutathione
 RT peroxidases.";
 RL Plant Mol. Biol. 21:923-927(1993).
 CC -1- FUNCTION: MAY CONSTITUTE A GLUTATHIONE PEROXIDASE-LIKE
 CC PROTECTIVE SYSTEM AGAINST OXIDATIVE STRESSES.
 CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized
 CC glutathione + 2 H(2)O.
 CC -1- INDUCTION: BY SALT STRESS.
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X66377; CAA47018.1; -.
 DR HSSP; P00435; 1GP1.
 DR InterPro: IPR000889; Glut_peroxidase.
 DR Pfam: PF00255; GSHPX; 1.
 DR PRINTS: PRO1011; GLUTPROXDASE.
 DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
 DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
 KW Oxidoreductase; Peroxidase.
 FT ACT_SITE 41 41
 FT 41 41 BY SIMILARITY.
 SQ SEQUENCE 167 AA; 18596 MW; DB6BDDC363F3260 CRC64;

Query Match 4.8%; Score 9; DB 1; Length 167;
 Best Local Similarity 100.0%; Pred. No. 0.079;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFCPNOFG 90
 DB 66 LAFCPNOFG 74

RESULT 7
 GSHC_SCHMA STANDARD; PRT; 169 AA.
 ID GSHC_SCHMA
 AC 000277;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Glutathione peroxidase (EC 1.11.1.9) (GPX).
 GN GPX1.
 OS Schistosoma mansoni (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;

RESULT	8			
ID	GSN2_NICSY	STANDARD:	PRT:	169 AA.
DT	01-APR-1993 (Rel. 25, Created)			
DT	01-APR-1993 (Rel. 25, last sequence update)			
DT	30-MAY-2000 (Rel. 39, last annotation update)			
DE	Glutathione peroxidase homology 6P229 (EC 1.11.1.9).			
OC	Nicotiana sylvestris (Wood tobacco).			
OC	Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
OC	Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.			
OX	NCBI_TaxId=4096;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Protoplast;			
RX	MEDLINE=92163033; PubMed=1536938;			
RA	Criqui M.C., Jamet E., Parmentier Y., Matbach J., Durr A., Fleck J.;			
RT	Isolation and characterization of a plant cDNA showing homology to			
RL	plant glutathione peroxidases. "			
	Plant Mol. Biol. 18:623-627(1992).			
CC	-1- FUNCTION: MAY CONSTITUTE A GLUTATHIONE PEROXIDASE-LIKE			
CC	PROTECTIVE SYSTEM AGAINST OXIDATIVE STRESSES.			
CC	-1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) - oxidized			
CC	glutathione + 2 H(2)O.			
CC	-1- TISSUE SPECIFICITY: GERMINATING SEED, APEX, FLOWER, AS WELL AS IN			
CC	STRESSED TISSUES.			
CC	-1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on test-			
CC	use by non-profit institutions as long as their content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL, X60219; CAA42780.1; -.			
DR	PIR, S20501; S20501.			
DR	HSSP, P00435; IGPI.			
DR	InterPro, IPR000889; Glut_peroxidase.			
DR	Pfam, PF00255; GSPx; 1.			
DR	PRINTS, PR01011; GUTPPROXDAE.			
DR	PROSITE, PS00460; GLUTATHIONE_PEROXID_1; 1.			
DR	PROSITE, PS00763; GLUTATHIONE_PEROXID_2; 1.			
KW	Oxidoreductase, Peroxidase.			
FT	ACT_SITE 43 .. 43 BY SIMILARITY.			
SEQ	SEQUENCE 169 AA; 18767 MW; 401919069E1E97C7 CRC64;			

Query Match	4.8%	Score 9;	DB 1;	Length 169;
Best Local Similarity	100.0%	Pred. No. 0.06;		
Matches	9;	Conservative	0;	Mismatches 0;
OY	82	LAFPCNCFG	90	
Db	68	LAFPCNCFG	76	
RESULT	9			
GSHY_HELAN				
ID	GSHY_HELAN	STANDARD;	PRT;	180 AA.
AC	O23968;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Glutathione peroxidase 2 (EC 1.11.1.9).			
GN	GPXHA-2.			
OS	Helianthus annuus (Common sunflower).			
OS	Eukaryota:			
OC	Viridiplantae:			
OC	Streptophyta:			
OC	Embryophyta:			
OC	Tracheophyta:			
OC	Spermatophyta:			
OC	eudicotyledons:			
OC	core eudicots:			
OC	Asteridae:			
OC	eunasterids II:			
OC	Asterales:			
OC	Asteraceae:			
OC	Asteroideae:			

OC Helianthae: Helianthus.
OX NCBI_TaxID=4232;
RN [1]
RP SEQUENCE FROM N.A.
RA Drevet J.R., Gagne G., Touryelle de Labroue D., Nicolas P.,
RA Dufure J.P., Ledoligt G., Roedel-Drevet P.;
RL Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MAY CONSTITUTE A GLUTATHIONE PEROXIDASE-LIKE
CC PROTECTIVE SYSTEM AGAINST OXIDATIVE STRESSES.
CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized
CC glutathione + 2 H(2)O
CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Y14707; CAA75009.1; -
DR HSSP: P00435; IGPI
DR InterPro: IPR000889; Glut_peroxidase.
DR Pfam: PF00255; GSHpx; 1.
DR PRINTS: PR01011; GLUTPROXDAE.
DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
DR Oxidoreductase; Peroxidase.
KW ACT_SITE 54 54
FT SEQUENCE 180 AA; 20174 MW; E3309DEAD2ADE0 CRC64;
SQ

Query Match 4.8%; Score 9; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.085; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

OY 82 LAEPCNOFG 90
DB 79 LAEPCNOFG 87

RESULT 10
GSHH_HUMAN
AC P36969; 043381;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Phospholipid hydroperoxide glutathione peroxidase, mitochondrial
DE precursor (EC 1.11.1.9) (PflGpx) (GPX-4).
GN GPX4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=94314239; PubMed=8039723;
RA Esworthy R.S., Doan K., Doroshov J.H., Chu F.-F.;
RT "Cloning and sequencing of the cDNA encoding a human testis
RT phospholipid hydroperoxide glutathione peroxidase.";
RL Gene 144:317-318(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98381025; PubMed=9705830;
RA Kehler M.J., Montoya M.A.;
RT "Structural organization of the human selenium-dependent phospholipid
RT hydroperoxide glutathione peroxidase gene (GPX4): chromosomal
RT localization to 19p13.3.";
RL Biochem. Biophys. Res. Commun. 249:53-55(1998).
RN [3]

RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stilaagen S.,
RA Phan H., Velasco N., Ganes J., Dangnan L., Poundstone P.,
RA Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andrelse T.,
RA Tranheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,
RA Bruce R., Thomas P., Quan G., Krommiller B., Arellano A.,
RA Montomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,
RA Carraro A.V.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: COULD PLAY A MAJOR ROLE IN PROTECTING MAMMALS FROM THE
CC TOXICITY OF INGESTED LIPID HYDROPEROXIDES.
CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized
CC glutathione + 2 H(2)O.
CC -1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS
CC ENCODED BY THE OPAL CODON, UGA.
CC -1- SUBCELLULAR LOCATION: Mitochondrial and cytoplasmic.
CC -1- ALTERNATIVE PRODUCTS: A SINGLE NUCLEAR GENE PRODUCES BOTH FORMS
CC BY USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
CC -1- TISSUE SPECIFICITY: PRESENT PRIMARILY IN TESTIS.
CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X71973; CAA50793.1; ALT_SEQ.
DR EMBL: AF060972; AAC32261.1; ALT_SEQ.
DR EMBL: AC004151; AAC03239.1; ALT_SEQ.
DR HSSP: P00435; IGPI.
DR MIM: 138322; -
DR InterPro: IPR000889; Glut_peroxidase.
DR Pfam: PF00255; GSHpx; 1.
DR PRINTS: PR01011; GLUTPROXDAE.
DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
DR Oxidoreductase; Peroxidase; Selenium; Selenocysteine;
KW Mitochondrion; Transl. peptide; Alternative initiation.
FT TRANSIT 1 197
FT CHAIN 1 197
FT CHAIN 28 197
FT INIT_MET 28 28
FT SE_CYS 73 73
FT SEQUENCE 197 AA; 22128 MW; 1AE3A2DAEC8FCBB1 CRC64;
SQ

Query Match 4.8%; Score 9; DB 1; Length 197;
Best Local Similarity 100.0%; Pred. No. 0.092; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

OY 82 LAEPCNOFG 90
DB 98 LAEPCNOFG 106

RESULT 11
GSHH_MOUSE
AC 070325;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phospholipid hydroperoxide glutathione peroxidase, mitochondrial
DE precursor (EC 1.11.1.9) (PflGpx) (GPX-4).
GN GPX4
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_Taxid=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BAIB/C, AND C57BL/6J; TISSUE=Testis, and Myocardium;
 RX MEDLINE=99272820; PubMed=10341094;
 RA Knopf E.A., Arndt T.L., Eng K.L., Caldwell M., Lebeuf R.C.,
 RA Deeb S.S., O'Brien K.D.;
 RT "Murine phospholipid hydroperoxide glutathione peroxidase: cDNA
 RT sequence, tissue expression, and mapping.";
 RL Mamm. Genome 10:601-605(1999)
 CC
 CC -1- FUNCTION: COULD PLAY A MAJOR ROLE IN PROTECTING MAMMALS FROM THE
 CC TOXICITY OF INGESTED LIPID HYDROPEROXIDES.
 CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized
 CC glutathione + 2 H(2)O.
 CC -1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS
 CC ENCODED BY THE OPAL CODON, UGA.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial and cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS: A SINGLE NUCLEAR GENE PRODUCES BOTH FORMS
 CC BY USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
 CC -1- TISSUE SPECIFICITY: PRESENT PRIMARILY IN TESTIS.
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF045768; AAC1832.1; ALT_INIT.
 DR EMBL: AF045769; AAC1833.1; ALT_INIT.
 DR EMBL: AF044056; AAC14560.1; -.
 DR HSSP: P00435; IGPI.
 DR MGD: MGI:104767; Gpx4.
 DR InterPro: IPR000889; Glut_peroxidase.
 DR Pfam: PF00255; GSHpx; 1.
 DR PRINTS: PRO1011; GLUTPROXDAE.
 DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
 DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
 KW Oxidoreductase; Peroxidase; Selenium; Selenocysteine;
 KW Mitochondrion; Transit peptide; Alternative initiation.
 FT TRANSIT 1 ?
 FT CHAIN ? 197
 FT CHAIN 197
 FT CHAIN 28 197
 FT CHAIN 28 197
 FT INIT_MET 28 28
 FT SE_CYS 73 73
 FT SE_CYS 73 73
 SQ SEQUENCE 197 AA; 22182 MW; 5CED5731AC24E51C CRC64;
 Query Match 4.8%; Score 9; DB 1; Length 197;
 Best Local Similarity 100.0%; Pred No. 0.092; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 82 LAFCNCFG 90
 DB 98 LAFCNCFG 106
 RESULT 12
 GSHH_PIG STANDARD; PRT; 197 AA.
 AC P36968;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Phospholipid hydroperoxide glutathione peroxidase, mitochondrial
 DE precursor (EC 1.11.1.9) (PHEpx) (GPX-4).
 GN GPX4.
 OS Sus scrofa (Pig).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 ON NCBI_Taxid=9823;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93312346; PubMed=8323565;
 RA Sunde R.A., Dyer J.A., Moran T., Evenson J.K., Sugimoto M.;
 RA "Phospholipid hydroperoxide glutathione peroxidase: full-length pig
 RT blastocyst cDNA sequence and regulation by selenium status.";
 RL Biochem. Biophys. Res. Commun. 193:905-911(1993).
 RN
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Liver, and Heart;
 RX MEDLINE=94171752; PubMed=8125951;
 RA Brigelius-Flohe R., Aumann K.-D., Bloecker H., Gross G.,
 RA Wingender E., Flohe L.;
 RA Koenig E., Flohe L.;
 RT "Phospholipid-hydroperoxide glutathione peroxidase. Genomic DNA,
 RT cDNA, and deduced amino acid sequence.";
 RL J. Biol. Chem. 269:7342-7348(1994).
 RN
 RN [3]
 RP SEQUENCE OF 40-197 FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=92137773; PubMed=1778506;
 RA Schuckelt R., Brigelius-Flohe R., Maiorino M., Roveri A., Reumkens J.,
 RA Strassburger W., Ursini F., Wolf B., Flohe L.;
 RT "Phospholipid hydroperoxide glutathione peroxidase is a selenoenzyme
 RT distinct from the classical glutathione peroxidase as evident from
 RT cDNA and amino acid sequencing.";
 RL Free Radic. Res. Commun. 14:343-361(1991).
 CC
 CC -1- FUNCTION: COULD PLAY A MAJOR ROLE IN PROTECTING MAMMALS FROM THE
 CC TOXICITY OF INGESTED LIPID HYDROPEROXIDES.
 CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized
 CC glutathione + 2 H(2)O.
 CC -1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS
 CC ENCODED BY THE OPAL CODON, UGA.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial and cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS: A SINGLE NUCLEAR GENE PRODUCES BOTH FORMS
 CC BY USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: L12743; AAA31099.2; -.
 DR EMBL: L12743; AAA31098.2; ALT_SEQ.
 DR EMBL: X76009; CAA53596.1; ALT_INIT.
 DR EMBL: X76008; CAA53595.1; ALT_INIT.
 DR EMBL: S80257; AAB21327.2; -.
 DR PIR: JN0608; JN0608.
 DR HSSP: P00435; IGPI.
 DR InterPro: IPR000889; Glut_peroxidase.
 DR Pfam: PF00255; GSHpx; 1.
 DR PRINTS: PRO1011; GLUTPROXDAE.
 DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
 DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
 KW Oxidoreductase; Peroxidase; Selenium; Selenocysteine;
 KW Mitochondrion; Transit peptide; Alternative initiation.
 FT TRANSIT 1 ?
 FT CHAIN ? 197
 FT CHAIN 197
 FT CHAIN 28 197
 FT CHAIN 28 197
 FT INIT_MET 28 28
 FT SE_CYS 73 73
 FT SE_CYS 73 73
 SQ SEQUENCE 197 AA; 22290 MW; 348645ABE35A7FD0 CRC64;

Query Match 4.8%; Score 9; DB 1; Length 197;
 Best Local Similarity 100.0%; Pred. No. 0.092;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFPCNOFG 90
 Db 98 LAFPCNOFG 106

RESULT 13

GSNH_RAT STANDARD; PRT; 197 AA.
 AC P36970;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Phospholipid hydroperoxide glutathione peroxidase, mitochondrial precursor (EC 1.11.1.9) (PDB: 1GPI).
 GN GPX4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE OF 21-197 FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
 RA Sunde R.A., Dyer J.A., Moran T.V., Evenson J.K.;
 RT "Rat liver phospholipid hydroperoxide glutathione peroxidase.";
 RL Submitted (Oct-1993) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Testis;
 RX MEDLINE=96070797; PubMed=7592947;
 RA Puspapa-Rekha T.R., Burdall A.L., Oleksa L.M., Chisolm G.M., Driscoll D.M.;
 RT "Rat phospholipid hydroperoxide glutathione peroxidase. cDNA cloning and identification of multiple transcription and translation start sites.";
 RL J. Biol. Chem. 270:26993-26999(1995).
 RN [3]
 RP SEQUENCE OF 17-197 FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
 RX MEDLINE=96318522; PubMed=8749327;
 RA Imai H., Sumi D., Hanamoto A., Arai M., Sugiyama A., Chiba N., Kuchino Y., Nakagawa Y.;
 RT "Molecular cloning and functional expression of a cDNA for rat phospholipid hydroperoxide glutathione peroxidase: 3'-untranslated region of the gene is necessary for functional expression.";
 RL J. Biochem. 118:1061-1067(1995).
 RN [4]
 RP CHARACTERIZATION.
 RC TISSUE=Testis;
 RA MEDLINE=92210587; PubMed=1556123;
 RX Koveri A., Casasco A., Maiorino M., Dalan P., Calligaro A., Ursini F.;
 RT "Phospholipid hydroperoxide glutathione peroxidase of rat testis. Gonadotropin dependence and immunocytochemical identification.";
 RL J. Biol. Chem. 267:6142-6146(1992).
 CC -1- FUNCTION: COULD PLAY A MAJOR ROLE IN PROTECTING MAMMALS FROM THE TOXICITY OF INGESTED LIPID HYDROPEROXIDES.
 CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized glutathione + 2 H(2)O.
 CC -1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS ENCODED BY THE OPAL CODON, UGA.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial and cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS: A SINGLE NUCLEAR GENE PRODUCES BOTH FORMS BY USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
 CC -1- TISSUE SPECIFICITY: PRESENT PRIMARILY IN TESTIS.
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL: U24896; AAA1842.2; ALT_INIT.
 DR EMBL: U37427; AAC52503.1; -
 DR EMBL: X82679; CAA57996.1; ALT_INIT.
 DR HSSP: P00435; IGPI.
 DR InterPro: IPR000889; Glut_peroxidase.
 DR Pfam: PF00255; GSHpx.1.
 DR PRINTS: PR01011; GLUTPEROXDASE.
 DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
 DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
 KW Oxidoreductase; Peroxidase; Selenium; Selenocysteine;
 KW Mitochondrion; Transil peptide; Alternative initiation.
 FT TRANSIT 1 197
 FT CHAIN ? 197
 FT CHAIN 28 197
 FT INIT_MET 28 28
 FT SE_CYS 73 73
 FT CONFLICT 45 45
 SQ SEQUENCE 197 AA; 22178 MW; 83FE1EBA52E2EE14 CRC64;
 A -> S (IN REF. 2).
 PEROXIDASE, CYTOPLASMIC ISOFORM.
 PHOSPHOLIPID HYDROPEROXIDE GLUTATHIONE
 PEROXIDASE, MITOCHONDRIAL ISOFORM.
 PHOSPHOLIPID HYDROPEROXIDE GLUTATHIONE
 PEROXIDASE, CYTOPLASMIC ISOFORM.

Query Match 4.8%; Score 9; DB 1; Length 197;
 Best Local Similarity 100.0%; Pred. No. 0.092;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFPCNOFG 90
 Db 98 LAFPCNOFG 106

RESULT 14

GSNH_ARATH STANDARD; PRT; 242 AA.
 AC P52032;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Glutathione peroxidase homolog, chloroplast precursor (EC 1.11.1.9).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RA Gachotte D., Benveniste P.;
 RT "Cloning and sequencing of a glutathione peroxidase homologue from Arabidopsis thaliana.";
 RL (In) Plant Gene Register PCR95-133.
 CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized glutathione + 2 H(2)O
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X89866; CAA61965.1; -
 DR HSSP: P00435; IGPI.
 DR InterPro: IPR000889; Glut_peroxidase.
 DR Pfam: PF00255; GSHpx.1.
 DR PRINTS: PR01011; GLUTPEROXDASE.

DR PROSITE; PS00460; GLUTATHIONE_PEROXID_1; 1.
 DR PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.
 KW Peroxidase; Oxidoreductase; Transit peptide; Chloroplast.
 FT TRANSIT 1 64 CHLOROPLAST (POTENTIAL).
 FT CHAIN 65 242 GLUTATHIONE_PEROXIDASE HOMOLOG.
 FT ACT_SITE 111 111 BY SIMILARITY.
 SQ SEQUENCE 242 AA; 26814 MW; 3A7031CCB416B857 CRC64;

Query Match 4.8%; Score 9; DB 1; Length 242;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFCNOFG 90
 |||||
 Db 136 LAFCNOFG 144

Query Match 4.3%; Score 8; DB 1; Length 221;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFCNOFG 89
 |||||
 Db 96 LAFCNOFG 103

Search completed: August 23, 2002, 14:42:08
 Job time: 130 sec

RESULT 15
 GSHU_DIRIM STANDARD; PRT; 221 AA.
 ID PS2033;
 AC 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Glutathione peroxidase precursor (EC 1.11.1.9) (DI29).
 OS Dicrofilaria immitis (Canine heartworm).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Splirurida; Filarioidea;
 OC Onchocercidae; Dicrofilaria.
 OX NCBI_TaxID=6287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Venkatakrisnaiah L., James E.;
 RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96162489; PubMed=9501847;
 RA Tripp C.A., Frank R.S., Selkirk M.E., Tang L., Mika-Grieve M.,
 RA Frank G.R., Grieve R.B.;
 RT "Dicrofilaria immitis: molecular cloning and expression of a cDNA
 encoding a selenium-independent secreted glutathione peroxidase.";
 RL Exp. Parasitol. 88:43-50(1998).
 CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized
 glutathione + 2 H(2)O.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Extracellular (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE_PEROXIDASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U04693; AAA16224.1; -;
 DR EMBL; U87457; AAB58573.1; -;
 DR EMBL; U87458; AAB58574.1; -;
 DR HSSP; P00435; 1GPI
 DR InterPro; IPR000889; Glut_peroxidase.
 DR Pfam; PF00255; GSHpx; 1.
 DR PRINTS; PRO1011; GLUTPROXDASE.
 DR PROSITE; PS00460; GLUTATHIONE_PEROXID_1; 1.
 DR PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.
 KW Oxidoreductase; Peroxidase; Glycoprotein; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 221 GLUTATHIONE_PEROXIDASE.
 FT ACT_SITE 72 72 BY SIMILARITY.
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 221 AA; 25453 MW; 88FF848D567CF28 CRC64;

